

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

Om protein - protein search, using sw model

Run on: May 19, 2006, 17:32:02 ; Search time 9 seconds
 (without alignments)
 0.949 Million cell updates/sec

Title: US-10-825-958-13
 Perfect score: 19
 Sequence: KLVF 4

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Post-processing: Minimum Match 0%
 Maximum DB seq length: 20000000
 Listing first 1000 summaries

Database : Published Applications AA_New/*

1: /EMC_Celerra_SIDS3_ptodata/2/pupbaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3_ptodata/2/pupbaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3_ptodata/2/pupbaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3_ptodata/2/pupbaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3_ptodata/2/pupbaa/US09_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3_ptodata/2/pupbaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3_ptodata/2/pupbaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3_ptodata/2/pupbaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 1s derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	19	100.0	5	US-10-520-386-2	Sequence 2, Appli
2	19	100.0	32	1 US-07-731-899-6	Sequence 6, Appli
3	19	100.0	40	1 US-07-731-899-6	Sequence 2, Appli
4	19	100.0	40	1 US-07-731-899-5	Sequence 5, Appli
5	19	100.0	40	1 US-11-104-300-3	Sequence 3, Appli
6	19	100.0	42	1 US-07-731-899-3	Sequence 3, Appli
7	19	100.0	42	7 US-11-104-300-2	Sequence 2, Appli
8	19	100.0	43	1 US-09-731-899-1	Sequence 4, Appli
9	19	100.0	59	1 US-09-731-899-1	Sequence 1, Appli
10	19	100.0	71	7 US-11-254-185-49	Sequence 49, Appli
11	19	100.0	123	7 US-11-254-185-29	Sequence 29, Appli
12	19	100.0	148	6 US-10-196-749-456	Sequence 456, Appli
13	19	100.0	254	7 US-11-167-773-57	Sequence 57, Appli
14	19	100.0	254	7 US-11-167-773-76	Sequence 57, Appli
15	19	100.0	282	7 US-11-251-466-46	Sequence 46, Appli
16	19	100.0	282	7 US-11-264-744-72	Sequence 72, Appli
17	19	100.0	294	6 US-10-505-928-33	Sequence 29, Appli
18	19	100.0	313	1 US-07-949-925-89	Sequence 89, Appli
19	19	100.0	344	6 US-10-505-928-652	Sequence 652, Appli
20	19	100.0	424	6 US-10-196-749-8	Sequence 8, Appli
21	19	100.0	448	6 US-10-975-692-15	Sequence 15, Appli
22	19	100.0	710	7 US-11-258-767-33	Sequence 33, Appli
23	19	100.0	711	7 US-11-258-767-12	Sequence 12, Appli
24	19	100.0	711	7 US-11-258-767-15	Sequence 15, Appli
25	19	100.0	711	7 US-11-258-767-17	Sequence 17, Appli

26 19 100.0 711 7 US-11-258-767-18
 Sequence 18, Appli
 Sequence 21, Appli
 Sequence 27, Appli
 Sequence 30, Appli
 Sequence 34, Appli
 Sequence 12, Appli
 Sequence 1, Appli
 Sequence 2992, App
 Sequence 471, App
 Sequence 100, App
 Sequence 145, App
 Sequence 141, App
 Sequence 63, Appli
 Sequence 31, Appli
 Sequence 478, App
 Sequence 51, Appli
 Sequence 178, App
 Sequence 42, Appli
 Sequence 2554, AP
 Sequence 1, Appli
 Sequence 244, AP
 Sequence 12, Appli
 Sequence 855, App
 Sequence 155, App
 Sequence 152, App
 Sequence 154, App
 Sequence 156, App
 Sequence 175, App
 Sequence 177, App
 Sequence 257, App
 Sequence 310, APP
 Sequence 4051, APP
 Sequence 5730, APP
 Sequence 6059, APP
 Sequence 10501, APP
 Sequence 1755, APP
 Sequence 1673, APP
 Sequence 1677, APP
 Sequence 835, APP
 Sequence 984, APP
 Sequence 1815, APP
 Sequence 475, APP
 Sequence 451, APP
 Sequence 744, APP
 Sequence 126, APP
 Sequence 127, APP
 Sequence 128, APP
 Sequence 132, APP
 Sequence 211, APP
 Sequence 221, APP
 Sequence 791, APP
 Sequence 98, APP
 Sequence 183, APP
 Sequence 2403, APP
 Sequence 3, APPi
 Sequence 3, Appli
 Sequence 365, APP
 Sequence 18, Appli
 Sequence 132, APP
 Sequence 4, Appli
 Sequence 1, Appli
 Sequence 32, Appli
 Sequence 65, Appli
 Sequence 763, APP
 Sequence 132, APP
 Sequence 367, APP
 Sequence 9, Appli
 Sequence 76, Appli
 Sequence 833, APP
 Sequence 496, APP
 Sequence 56, APP
 Sequence 16, APP
 Sequence 468, APP
 Sequence 17, APP
 Sequence 58, APP
 Sequence 18, APP
 Sequence 400, APP

99	16	84.2	502	7	US-11-311-555-12	Sequence 12, App	172	15	78.9	352	6	US-10-511-937-2412
100	16	84.2	502	7	US-11-311-561-12	Sequence 12, App	173	15	78.9	372	7	US-11-251-465-71
101	16	84.2	502	7	US-11-101-316-158	Sequence 158, App	174	15	78.9	392	6	US-10-511-937-2583
102	16	84.2	526	7	US-11-024-544A-14	Sequence 12, App	175	15	78.9	407	6	US-10-511-937-16
103	16	84.2	526	7	US-11-190-750-80	Sequence 14, App	176	15	78.9	415	6	US-10-511-937-2993
104	16	84.2	526	7	US-11-190-750-84	Sequence 80, App	177	15	78.9	442	7	US-11-289-989-6
105	16	84.2	526	7	US-11-264-784-82	Sequence 84, App	178	15	78.9	442	7	US-11-289-989-16
106	16	84.2	542	6	US-10-196-749-398	Sequence 82, App	179	15	78.9	457	6	US-10-196-749-48
107	16	84.2	560	6	US-10-468-193-34	Sequence 398, App	180	15	78.9	457	7	US-11-101-316-12
108	16	84.2	811	6	US-10-511-937-2584	Sequence 34, App	181	15	78.9	459	6	US-10-505-928-461
109	16	84.2	673	6	US-10-505-928-551	Sequence 551, App	182	15	78.9	474	6	US-10-982-908-14
110	16	84.2	737	6	US-10-505-928-123	Sequence 123, App	183	15	78.9	474	6	US-10-982-908-16
111	16	84.2	821	6	US-10-505-928-316	Sequence 608, App	184	15	78.9	475	6	US-10-505-928-142
112	16	84.2	864	7	US-11-312-797-2	Sequence 2, App	185	15	78.9	475	7	US-10-982-908-12
113	16	84.2	951	6	US-10-199-229-9	Sequence 9, App	186	15	78.9	475	7	US-11-251-959-9
114	16	84.2	951	6	US-10-199-229-13	Sequence 13, App	187	15	78.9	480	6	US-10-186-749-82
115	16	84.2	967	6	US-10-505-928-95	Sequence 2584, App	188	15	78.9	481	7	US-11-249-111-77
116	16	84.2	820	6	US-10-982-908-26	Sequence 26, App	189	15	78.9	500	7	US-11-251-959-6
117	16	84.2	821	6	US-10-505-928-505	Sequence 316, App	190	15	78.9	500	7	US-11-024-544A-172
118	16	84.2	864	7	US-10-511-937-2566	Sequence 2566, App	191	15	78.9	500	7	US-11-190-750-140
119	16	84.2	951	6	US-10-199-229-13	Sequence 37, App	192	15	78.9	505	7	US-11-251-959-12
120	16	84.2	967	6	US-10-505-928-95	Sequence 795, App	193	15	78.9	505	7	US-11-242-111-28
121	16	84.2	995	7	US-11-246-999-48	Sequence 48, App	194	15	78.9	506	6	US-10-505-928-135
122	16	84.2	1025	6	US-10-505-928-505	Sequence 505, App	195	15	78.9	506	6	US-11-101-316-124
123	16	84.2	1186	6	US-10-511-937-2566	Sequence 2566, App	196	15	78.9	511	7	US-11-305-670-56
124	16	84.2	1457	7	US-11-280-757-37	Sequence 37, App	197	15	78.9	542	7	US-11-227-61-2
125	16	84.2	1539	6	US-10-511-937-2545	Sequence 2545, App	198	15	78.9	542	7	US-11-227-61-4
126	16	84.2	1822	6	US-10-505-928-700	Sequence 700, App	199	15	78.9	582	6	US-10-505-928-813
127	16	84.2	1842	7	US-10-511-931-2929	Sequence 2929, App	200	15	78.9	587	6	US-10-511-931-2407
128	16	84.2	209	7	US-11-301-934-1903	Sequence 1903, App	201	15	78.9	643	6	US-10-504-120-19
129	16	84.2	2351	7	US-11-183-218-30	Sequence 30, App	202	15	78.9	648	6	US-11-305-670-56
130	16	84.2	2351	7	US-11-280-757-35	Sequence 35, App	203	15	78.9	653	6	US-11-227-61-2
131	16	84.2	4590	6	US-10-505-928-650	Sequence 569, App	204	15	78.9	694	7	US-10-505-928-650
132	16	84.2	8	6	US-10-538-066-660	Sequence 660, App	205	15	78.9	699	6	US-10-196-749-138
133	16	84.2	1842	7	US-10-511-931-2929	Sequence 321, App	206	15	78.9	708	6	US-10-196-749-584
134	16	84.2	209	7	US-10-538-066-321	Sequence 322, App	207	15	78.9	769	6	US-10-504-120-19
135	15	84.2	2351	7	US-10-538-066-49	Sequence 649, App	208	15	78.9	777	6	US-10-511-814-14
136	15	84.2	10	6	US-10-538-066-24	Sequence 24, App	209	15	78.9	806	6	US-10-505-920-211
137	15	84.2	10	6	US-10-505-928-650	Sequence 650, App	210	15	78.9	825	6	US-10-511-937-301
138	15	84.2	11	6	US-10-538-066-21	Sequence 21, App	211	15	78.9	825	6	US-10-511-937-325
139	15	84.2	13	6	US-10-538-066-651	Sequence 651, App	212	15	78.9	846	6	US-10-505-928-300
140	15	84.2	68	1	US-03-949-925-327	Sequence 116, App	213	15	78.9	850	6	US-10-511-937-2573
141	15	84.2	78.9	9	US-10-982-908-22	Sequence 22, App	214	15	78.9	1052	6	US-10-497-088-21
142	15	84.2	76	7	US-11-251-673-1	Sequence 1, App	215	15	78.9	1346	6	US-11-231-465-22
143	15	84.2	85	6	US-10-501-834-9	Sequence 9, App	216	15	78.9	178.9	6	US-10-511-937-2968
144	15	84.2	94	6	US-10-505-928-36	Sequence 36, App	217	15	78.9	3113	6	US-10-505-928-325
145	15	84.2	144	7	US-11-301-554-327	Sequence 327, App	218	14	73.7	10	7	US-11-238-341-40
146	15	84.2	152	6	US-10-511-937-2442	Sequence 2442, App	219	14	73.7	15	6	US-11-40-497-088-21
147	15	84.2	152	7	US-11-301-554-787	Sequence 787, App	220	14	73.7	15	6	US-11-140-487A-2095
148	15	84.2	152	7	US-11-301-554-795	Sequence 795, App	221	14	73.7	222	14	73.7
149	15	84.2	164	6	US-10-505-928-706	Sequence 706, App	222	14	73.7	223	14	73.7
150	15	84.2	164	6	US-10-511-814-4	Sequence 4, App	223	14	73.7	224	14	73.7
151	15	84.2	164	7	US-11-242-111-26	Sequence 26, App	224	14	73.7	225	14	73.7
152	15	84.2	166	6	US-10-538-066-761	Sequence 761, App	226	14	73.7	226	14	73.7
153	15	84.2	197	6	US-10-511-937-2611	Sequence 2611, App	227	14	73.7	227	14	73.7
154	15	84.2	197	7	US-11-196-749-448	Sequence 448, App	228	14	73.7	228	14	73.7
155	15	84.2	197	7	US-11-311-555-4	Sequence 4, App	229	14	73.7	229	14	73.7
156	15	84.2	197	7	US-11-311-555-4	Sequence 4, App	230	14	73.7	230	14	73.7
157	15	84.2	222	7	US-11-257-062-34	Sequence 34, App	231	14	73.7	231	14	73.7
158	15	84.2	231	7	US-11-249-111-116	Sequence 116, App	232	14	73.7	232	14	73.7
159	15	84.2	253	7	US-11-249-111-111	Sequence 111, App	233	14	73.7	233	14	73.7
160	15	84.2	258	6	US-10-505-928-497	Sequence 497, App	234	14	73.7	234	14	73.7
161	15	84.2	300	6	US-10-196-749-492	Sequence 492, App	235	14	73.7	235	14	73.7
162	15	84.2	313	7	US-11-257-062-48	Sequence 48, App	236	14	73.7	236	14	73.7
163	15	84.2	314	6	US-10-538-066-365	Sequence 365, App	237	14	73.7	237	14	73.7
164	15	84.2	314	6	US-10-538-066-366	Sequence 366, App	238	14	73.7	238	14	73.7
165	15	84.2	323	6	US-10-505-928-497	Sequence 497, App	239	14	73.7	239	14	73.7
166	15	84.2	325	7	US-11-264-784-65	Sequence 499, App	240	14	73.7	240	14	73.7
167	15	84.2	330	6	US-10-196-749-492	Sequence 500, App	241	14	73.7	241	14	73.7
168	15	84.2	331	7	US-11-190-750-30	Sequence 30, App	242	14	73.7	242	14	73.7
169	15	84.2	331	7	US-11-264-784-66	Sequence 36, App	243	14	73.7	243	14	73.7
170	15	84.2	345	7	US-11-249-111-155	Sequence 65, App	244	14	73.7	244	14	73.7
171	15	84.2	345	7	US-10-511-937-2609	Sequence 2609, App	245	14	73.7	245	14	73.7

GenCore version 5.1.8
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OM protein - protein search, using sw model
Run on: May 19, 2006, 17:20:21 ; Search time 196 Seconds
(without alignments)
9.331 Million cell updates/sec

Title: US-10-825-958-13
Perfect score: 19

Sequence: KLVF 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5
Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database : A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004as:*
- 9: geneseqp2005as:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	19	100.0	4	2 AAW45956	Aaw45956 Amyloid b
2	19	100.0	4	3 AAY7936	Aay7936 Beta-amyl
3	19	100.0	4	4 ARB48487	Abi8487 Antifibri
4	19	100.0	4	4 ARB48479	Abi8479 Antifibri
5	19	100.0	4	4 ARB8635	Abi8635 All-D pep
6	19	100.0	4	4 ARB8627	Abi8627 All-D pep
7	19	100.0	5	5 ARB9615	Aau6815 Amyloid t
8	19	100.0	4	5 AAW9623	Aau6823 Amyloid t
9	19	100.0	4	5 ARU11661	Aau11661 Peptide #
10	19	100.0	4	5 ARU11653	Aau11653 Peptide #
11	19	100.0	4	6 AAE35442	Aae35442 Abeta pep
12	19	100.0	4	6 ARB35449	Aae35449 Abeta pep
13	19	100.0	4	6 ARD3766	Adq3766 Vaccine a
14	19	100.0	4	8 ADQ37384	Adq37384 Amyloid-b
15	19	100.0	4	8 ADQ37326	Adq37326 Antifibri
16	19	100.0	4	8 ADQ37318	Adq37318 Antifibri
17	19	100.0	4	8 ADQ37274	Adq37274 Vaccine a
18	19	100.0	4	9 ADY37925	Ady37925 Amyloid-t
19	19	100.0	4	9 ADY37933	Ady37933 Amyloid-t
20	19	100.0	4	9 AEA22038	Aea22038 Human Abe
21	19	100.0	5	2 ARR7922	Aar7922 Test Ppt
22	19	100.0	5	2 AAW2215	Aaw2215 Beta-amyl
23	19	100.0	5	2 AAW45933	Aaw45933 Partial s

Aaa45966 Peptide d	24	19	100.0	5	2 AAW45966
Aaa45950 Amyloid b	25	19	100.0	5	2 AAW45950
Aab29089 A-beta-bi	26	19	100.0	5	2 AAW29089
Aab89367 Beta-amyl	27	19	100.0	5	2 AAW89367
Aay79367 Beta-amyl	28	19	100.0	5	3 AAY79367
Aab6279 Residues	29	19	100.0	5	4 AAB6279
Aab68489 Antifibri	30	19	100.0	5	4 AAB68489
Aab68481 Antifibri	31	19	100.0	5	4 AAB68481
Aab82637 All-D pep	32	19	100.0	5	4 AAB82637
Aab82629 All-D pep	33	19	100.0	5	4 AAB82629
Aab62803 Residues	34	19	100.0	5	4 AAB62803
Abi71010 Long form	35	19	100.0	5	5 ABG71010
Aab6847 Beta-amyl	36	19	100.0	5	5 AAC05847
Abi605183 Beta amyl	37	19	100.0	5	5 ABB05183
Abi82632 Abeta fib	38	19	100.0	5	5 AAB82632
Aab6825 Amyloid t	39	19	100.0	5	5 AAU96825
Aab6817 Beta pep	40	19	100.0	5	5 AAU96817
Aab84001 Transglut	41	19	100.0	5	5 AAB84001
Aau11655 Peptide #	42	19	100.0	5	5 AAU11655
Aau11663 Peptide #	43	19	100.0	5	5 AAU11663
Abi82632 Abeta fib	44	19	100.0	5	5 ABB82632
Aab35444 Abeta pep	45	19	100.0	5	5 AAE35444
Aab35451 Abeta pep	46	19	100.0	5	5 AAE35451
Abi43903 Beta-amyl	47	19	100.0	5	5 ABR43903
Adf60931 C-terminal	48	19	100.0	5	5 ADF60931
Adj71329 Pathologi	49	19	100.0	5	5 ADJ71329
Adj64061 Human bet	50	19	100.0	5	5 ADJ64061
Adm97741 Amyloid b	51	19	100.0	5	5 ADM97741
Adm64923 Amyloid b	52	19	100.0	5	5 ADM97741
Adg37328 Antifibri	53	19	100.0	5	5 ADG37328
Adg37276 Vaccine a	54	19	100.0	5	5 ADG37276
Adg37354 Beta-amyl	55	19	100.0	5	5 ADG37354
Adg37268 Vaccine a	56	19	100.0	5	5 ADG37268
Adg37320 Antifibri	57	19	100.0	5	5 ADG37320
Adg37320 Amyloid-b	58	19	100.0	5	5 ADG37320
Adg37382 Amyloid-b	59	19	100.0	5	5 ADG37382
Adg37382 Amyloid-t	60	19	100.0	5	5 ADY37927
Adg37935 Amyloid-t	61	19	100.0	5	5 ADY37935
Adg5195 Human amy	62	19	100.0	5	5 ADZ5195
Aee2307 Human Abe	63	19	100.0	5	5 AEE2307
Aee28520 Short amy	64	19	100.0	5	5 AED28520
Aee64847 A-alpha f	65	19	100.0	5	5 AER64847
Aaw02331 Beta-amyl	66	19	100.0	6	6 AAW02331
Aaw02314 Beta-amyl	67	19	100.0	6	6 AAW02314
Aaw45945 Amyloid b	68	19	100.0	6	6 AAW45945
Aaw45944 Amyloid b	69	19	100.0	6	6 AAW45944
Aaw29092 A-beta-bi	70	19	100.0	6	6 AAW29092
Aaw29091 A-beta-bi	71	19	100.0	6	6 AAW29091
Aat29090 A-beta-bi	72	19	100.0	6	6 AAW29090
Aav89378 Beta-amyl	73	19	100.0	6	6 AAW89378
Aav89377 Beta-amyl	74	19	100.0	6	6 AAW89377
Aav89388 Beta-amyl	75	19	100.0	6	6 AAW89388
Aab89388 Beta-amyl	76	19	100.0	6	6 AAW89388
Aab48484 Antifibri	77	19	100.0	6	6 AAB48484
Aab48475 Antifibri	78	19	100.0	6	6 AAB48475
Aab48496 Antifibri	79	19	100.0	6	6 AAB48496
Aab82654 All-D pep	80	19	100.0	6	6 AAB82654
Aab82657 All-D pep	81	19	100.0	6	6 AAB82657
Aab82660 All-D pep	82	19	100.0	6	6 AAB82660
Aab82663 All-D pep	83	19	100.0	6	6 AAB82663
Aab82651 All-D pep	84	19	100.0	6	6 AAB82651
Aab82632 All-D pep	85	19	100.0	6	6 AAB82632
ABG71031 Long form	86	19	100.0	6	6 ABG71031
Abg71009 Long form	87	19	100.0	6	6 ABG71009
Abg71008 Long form	88	19	100.0	6	6 ABG71008
Abg82663 All-D pep	89	19	100.0	6	6 ABB05177
Abg82651 All-D pep	90	19	100.0	6	6 ABB05177
Abg82657 All-D pep	91	19	100.0	6	6 ABB05176
Abg82632 All-D pep	92	19	100.0	6	6 ABB05177
Abg82632 All-D pep	93	19	100.0	6	6 ABB05189
Abg82632 All-D pep	94	19	100.0	6	6 ABB05189
Abg82632 All-D pep	95	19	100.0	6	6 ABB05189
Abg82632 All-D pep	96	19	100.0	6	6 ABB05189

GenCore version 5.1.8
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OM protein - protein search, using sw model
 Run on: May 19, 2006, 17:20:33 ; Search time 297 Seconds
 (without alignments)

12.458 Million cell updates/sec
 Title: US-10-825-958-13
 Perfect score: 19
 Sequence: 1 KLVF 4

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : UniProt 7.2:
 1: uniprot_sprot:
 2: uniprot_trembl:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match Length	DB ID	Description
1	19	Q8INSG_HUMAN	14	2 Q8iws6	hom sapien
2	19	Q9UH91_HUMAN	14	2 Q9UH91	homo sapien
3	19	Q4XV14_PLAUCH	2	Q4XV14	plasmidium
4	19	Q692Y3_SOYBE	2	Q692Y3	glycine max
5	19	Q9UWGB_9EGRY	27	2 Q9UWGB	thermococcus
6	19	Q4N1Z6_THEPRA	28	2 Q4N1Z6	theilleria p
7	19	Q7RAW5_PLAYO	28	2 Q7RAW5	plasmidium
8	19	Q7RNL4_PLAYO	2	Q7RNL4	playo
9	19	Q4DR54_TEENQ	29	2 Q4DR54	tetradon n
10	19	Q7RSH4_PLAYO	31	2 Q7RSH4	playo
11	19	Q47XC8_COLP3	31	2 Q47XC8	colwellia p
12	19	Q9IC33_HUMAN	33	2 Q9IC33	homo sapien
13	19	Q4XZD2_PLAUCH	35	2 Q4XZD2	plasmidium
14	19	Q4YX98_PLAUCH	38	2 Q4YX98	plauch
15	19	Q72988_SCHPO	39	2 Q72988	schipoo
16	19	Q7RWS3_PLAYO	39	2 Q7RWS3	playo
17	19	Q8BQG3_MOUSE	39	2 Q8BQG3	mouse
18	19	Q4YXK8_PLAUCH	41	2 Q4YXK8	plauch
19	19	Q8KEH6_CHLTH	41	2 Q8KEH6	chlth
20	19	Q56J56_GRAGR	42	2 Q56J56	gragr
21	19	Q76GUT7_TURTR	42	2 Q76GUT7	turtr
22	19	Q7M088_CAVPO	42	2 Q7M088	cavpo
23	19	Q8AXZ2_ICTPU	42	2 Q8AXZ2	ictpus
24	19	Q3VNU9_9CHLB	43	2 Q3VNU9	9chlb
25	19	Q4YH5_PLAUCH	44	2 Q4YH5	plauch
26	19	Q856G0_9GRAD	44	2 Q856G0	9grad
27	19	Q72zB2_BACCI	45	2 Q72zB2	bacchi
28	19	Q54555_9EURY	47	2 Q54555	9eury
29	19	Q54MRO_DICDI	48	2 Q54MRO	dicdi
30	19	Q9GR26_APHC0	48	2 Q9GR26	aphc0
31	19	Q3DG01_STRAGC	50	2 Q3DG01	stragc

32	19	100.0	50	2	Q3XXS7_ENTRC
33	19	100.0	51	2	Q416Z7_PLAUCH
34	19	100.0	51	2	Q4Vkd5_9EUC4
35	19	100.0	51	2	Q4VKF5_9EUC4
36	19	100.0	51	2	Q72AS1_DESVH
37	19	100.0	51	2	Q8QMN2_COWPV
38	19	100.0	52	2	Q8RIZ9_HUMAN
39	19	100.0	52	2	Q7RGW2_PLAUYO
40	19	100.0	52	2	Q8MEHO_9EUC4
41	19	100.0	53	2	Q7M1NT_SOYBN
42	19	100.0	53	2	Q2SMU7_9GAMM
43	19	100.0	53	2	Q5NMx2_RICCN
44	19	100.0	54	2	Q4X433_PLAUCH
45	19	100.0	54	2	Q8RBV2_THETN
46	19	100.0	55	1	A4_USRHA
47	19	100.0	55	1	A4_BOVIN
48	19	100.0	55	2	Q7UFC9_RHOB9
49	19	100.0	55	2	Q21IT0_RICCN
50	19	100.0	58	1	A4_CANFA
51	19	100.0	58	1	A4_RABBIT
52	19	100.0	58	1	A4_SHEEP
53	19	100.0	58	2	Q3J633_9CALI
54	19	100.0	59	1	A4_BOVIN
55	19	100.0	59	2	Q3HZT1_CAPNU
56	19	100.0	59	2	Q4T197_TEETING
57	19	100.0	60	2	Q8KDI1_BACAN
58	19	100.0	60	2	Q6ff025_BACAN
59	19	100.0	60	2	Q4RUF7_TEETING
60	19	100.0	61	2	Q3LSR5_SHIBIS
61	19	100.0	61	2	Q3YTD0_SHIHS
62	19	100.0	61	2	Q3YVXT7_SHIHS
63	19	100.0	61	2	Q2Nk03_9MOLU
64	19	100.0	61	2	Q9AFZ0_SHIFLU
65	19	100.0	62	2	Q4YEMO_PLABE
66	19	100.0	62	2	Q3HZT8_CAPNU
67	19	100.0	62	2	Q3W6C9_9VIRU
68	19	100.0	63	2	Q302AB_STRSU
69	19	100.0	63	2	Q89829_BALBO
70	19	100.0	63	2	Q8iCQ6_GADEN
71	19	100.0	63	2	Q8SPJ7_PIG
72	19	100.0	64	2	Q3NHY7_DRDOME
73	19	100.0	64	2	Q8NRY7_DRDOME
74	19	100.0	64	2	Q3MQ25_ANTST
75	19	100.0	64	2	Q8B457_PELLD
76	19	100.0	64	2	Q3GCl1_9CHLB
77	19	100.0	64	2	Q43gcl_CHLORBL
78	19	100.0	64	2	Q72qz9_leptospira
79	19	100.0	65	2	Q8f4t7_leptospira
80	19	100.0	65	2	Q41444_CAEEL
81	19	100.0	65	2	Q4Te84_TEETING
82	19	100.0	66	2	Q2H2S1_9ETTA
83	19	100.0	66	2	Q2H2S2_CAPSI
84	19	100.0	66	2	Q2H2S7_CAPSI
85	19	100.0	66	2	Q2H2T7_CAPNU
86	19	100.0	66	2	Q2H2T9_CAPNU
87	19	100.0	66	2	Q2H2U1_CAPCY
88	19	100.0	66	2	Q2h2s1_capra_pyrn
89	19	100.0	66	2	Q2h2s2_capra_sibir
90	19	100.0	66	2	Q2h2s7_capra_sibir
91	19	100.0	66	2	Q2h2t7_capra_nubia
92	19	100.0	66	2	Q2h2t9_capra_nubia
93	19	100.0	66	2	Q2h2u1_capra_cylin
94	19	100.0	67	2	Q2h2u2_capra_cauca
95	19	100.0	67	2	Q2h2u4_CAPCU
96	19	100.0	67	2	Q2h2u5_9ETTA
97	19	100.0	67	2	Q2h2u6_ACIDAD
98	19	100.0	67	2	Q2dt17_STRMU
99	19	100.0	67	2	Q3Pym6_NITHA
100	19	100.0	67	2	Q512m7_GBCOKA
101	19	100.0	67	2	Q92if4_rickettsia
102	19	100.0	67	2	Q7OHu9_PRVKA
103	19	100.0	68	2	Q7ram0_PLAVYA
104	19	100.0	68	2	Q8dt17_streptococc
105	19	100.0	68	2	Q3Pym6_nitrobacter
106	19	100.0	68	2	Q512m7_geobacillus
107	19	100.0	68	2	Q92if4_rickettsia
108	19	100.0	68	2	Q7OHu9_pseudoribofl
109	19	100.0	68	2	Q7ram0_plasmidium
110	19	100.0	68	2	Q6zou8_oryza_sativ
111	19	100.0	69	1	S61G3_ARATH
112	19	100.0	69	1	Q9q2zz_leimana
113	19	100.0	69	1	Q4x4t4_Plach
114	19	100.0	70	2	Q9dr18_Plach
115	19	100.0	70	2	Q9Hn03_BACHK
116	19	100.0	71	2	Q49rt5_mycolasma
117	19	100.0	71	2	Q3J7f7_burkholderi
118	19	100.0	71	2	Q5f7s4_neisseria_g

106	19	100.0	71	2.	063TA0_BURRPS	Q63IA0_burkholderi
107	19	100.0	72	2.	08UCT6_ARGTS	Q8UIC6_agrobacteri
108	19	100.0	72	2.	06CKD3_YARCI	Q6CK3_yarrowia_li
109	19	100.0	73	2.	025925_PLAFA	Q25925_plasmodium
110	19	100.0	73	2.	07P9F5_RICST	Q7P9F5_rickettsia
111	19	100.0	73	2.	07MV83_PORCT	Q7MV83_porphomon
112	19	100.0	73	2.	05ICP6_9ADEN	Q51P6_human_adeno
113	19	100.0	73	2.	05ICP7_9ADEN	Q51P7_human_adeno
114	19	100.0	74	2.	046109_DROMI	Q46109_drosophila
115	19	100.0	74	2.	05CJH6_CRYHO	Q5ch6_cryptospori
116	19	100.0	74	2.	05BQ60_STAU9	Q5bq60_staphylococ
117	19	100.0	74	2.	05BQ57_9ADEN	Q5bq57_untyped_hum
118	19	100.0	74	2.	05ICP5_9ADEN	Q51P5_human_adeno
119	19	100.0	74	2.	05ICP7_9ADEN	Q51P7_human_adeno
120	19	100.0	75	2.	081UQ0_BACAN	Q81UQ0_bacillus_an
121	19	100.0	75	2.	05BQ60_9ADEN	Q5bq60_untyped_hum
122	19	100.0	75	2.	05BQ62_9ADEN	Q5bq62_untyped_hum
123	19	100.0	75	2.	05ICP9_9ADEN	Q51P9_human_adeno
124	19	100.0	75	2.	05ICQ7_9ADEN	Q51q7_human_adeno
125	19	100.0	76	2.	05K2V4_LIMST	Q5K2V4_lymnaea_sta
126	19	100.0	76	2.	08VVM4_ECOLI	Q8VVM4_escherichia
127	19	100.0	76	2.	05BQ52_9ADEN	Q5bq52_untyped_hum
128	19	100.0	76	2.	05BQ53_9ADEN	Q5bq53_untyped_hum
129	19	100.0	76	2.	05ICP3_9ADEN	Q51P3_human_adeno
130	19	100.0	76	2.	05ICR0_9ADEN	Q51r0_human_adeno
131	19	100.0	76	2.	09TBS2_TOXRU	Q9tbs2_toxostoma_r
132	19	100.0	76	2.	09TBS6_9PASS	Q9tbs6_toxostoma_1
133	19	100.0	77	2.	054879_STREN	Q54879_streptococc
134	19	100.0	77	2.	05Q488_9ADEN	Q5bq48_untyped_hum
135	19	100.0	77	2.	05BQ55_9ADEN	Q5bq55_untyped_hum
136	19	100.0	77	2.	05BQ64_9ADEN	Q5bq64_untyped_hum
137	19	100.0	77	2.	05ICP2_9ADEN	Q51P2_human_adeno
138	19	100.0	77	2.	05ICP7_9ADEN	Q51P7_human_adeno
139	19	100.0	77	2.	05ICB8_9ADEN	Q51cb8_human_adeno
140	19	100.0	77	2.	05ICQ0_9ADEN	Q51cq0_human_adeno
141	19	100.0	77	2.	05ICR3_9ADEN	Q51r3_human_adeno
142	19	100.0	77	2.	09HPRI_HALSA	Q9hpri_halobacteri
143	19	100.0	77	2.	05ICR8_9ADEN	Q51r8_human_adeno
144	19	100.0	77	2.	05ICSI_9ADEN	Q5icsi_human_adeno
145	19	100.0	77	2.	05IC53_9ADEN	Q5ic53_human_adeno
146	19	100.0	77	2.	05IC66_ADE17	Q5ic66_human_adeno
147	19	100.0	77	2.	05IC73_9ADEN	Q5ic73_human_adeno
148	19	100.0	77	2.	05ICR1_9ADEN	Q51r1_human_adeno
149	19	100.0	78	2.	06BXN0_DEBHA	Q6bxn0_debaromyce
150	19	100.0	78	2.	06IG25_DRONE	Q6ig25_drosophilila
151	19	100.0	78	2.	03Y5V2_CITLIA	Q3y5v2_citrullus_1
152	19	100.0	78	2.	05BQ56_9ADEN	Q5bq56_untyped_hum
153	19	100.0	78	2.	05ICQ8_ADD35	Q51cq8_human_adeno
154	19	100.0	78	2.	05IC55_ADE18	Q5ic55_human_adeno
155	19	100.0	78	2.	05IC58_ADD35	Q5ic58_human_adeno
156	19	100.0	78	2.	05IC71_ADD32	Q5ic71_human_adeno
157	19	100.0	79	2.	0969F3_HUMAN	Q96f3_homo_sapien
158	19	100.0	79	2.	071102_LADDL	Q71102_lactobacilli
159	19	100.0	79	2.	05HMRO_STBLQ	Q5hmro_staphylococ
160	19	100.0	79	2.	081YZ4_BACAN	Q81yz4_bacillus_an
161	19	100.0	79	2.	092GFT7_RICCN	Q92gft7_rickettsia
162	19	100.0	79	2.	034543_CRGCR	Q34543_cricketulua
163	19	100.0	79	2.	05BQ51_9ADEN	Q5bq51_untyped_hum
164	19	100.0	79	2.	05IC09_9ADEN	Q51co9_human_adeno
165	19	100.0	79	2.	05IC52_9ADEN	Q51c52_human_adeno
166	19	100.0	80	2.	05BQ52_SCWTA	Q5bq52_schistosoma
167	19	100.0	80	2.	02SLP8_9GAMM	Q2slp8_hahella_che
168	19	100.0	80	2.	03Y020_ENTRFC	Q3y020_enterococcus
169	19	100.0	80	2.	063383_BACZ	Q63383_bacillus_ce
170	19	100.0	80	2.	05IC08_9ADEN	Q51co8_human_adeno
171	19	100.0	80	2.	05IC05_9ADEN	Q51co5_human_adeno
172	19	100.0	80	2.	05ICB9_9ADEN	Q51cb9_human_adeno
173	19	100.0	80	2.	05IC50_9ADEN	Q51c50_human_adeno
174	19	100.0	80	2.	05IC54_9ADEN	Q51c54_human_adeno
175	19	100.0	80	2.	05IC02_9ADEN	Q51co2_human_adeno
176	19	100.0	80	2.	05IC01_9ADEN	Q51co1_human_adeno
177	19	100.0	81	2.	096133_PLAF7	Q96133_plasmidium

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OM protein - protein search, using SW model
 Run on: May 19, 2006, 17:24:34 ; Search time 38 Seconds
 (without alignment)
 10.128 Million cell updates/sec

Title: US-10-825-958-13
 Perfect score: 19
 Sequence: 1 KLVF 4

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 80;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	19	100.0	16	T-cell receptor al
2	19	100.0	26	T-cell receptor de
3	19	100.0	29	T-cell receptor al
4	19	100.0	30	T-cell receptor de
5	19	100.0	31	F3461
6	19	100.0	32	A32302
7	19	100.0	32	D3502
8	19	100.0	32	D3461
9	19	100.0	33	A3461
10	19	100.0	33	E33502
11	19	100.0	33	B32540
12	19	100.0	33	I3461
13	19	100.0	33	B3461
14	19	100.0	33	S23194
15	19	100.0	34	C3461
16	19	100.0	34	H3461
17	19	100.0	34	I32502
18	19	100.0	36	C32502
19	19	100.0	36	H33502
20	19	100.0	36	A33540
21	19	100.0	42	PN0512
22	19	100.0	47	PC4133
23	19	100.0	53	PS0009
24	19	100.0	57	A60045
25	19	100.0	57	F60045
26	19	100.0	57	D60045
27	19	100.0	57	B60045
28	19	100.0	57	G60045
29	19	100.0	57	B60045

30	19	100.0	57	hypothetical prote
31	19	100.0	67	hypothetical prote
32	19	100.0	69	protein translocat
33	19	100.0	72	peptidyl-dipeptida
34	19	100.0	71	hypothetical prote
35	19	100.0	72	major merozoite su
36	19	100.0	73	rab protein Rab -
37	19	100.0	75	T-cell receptor al
38	19	100.0	78	hypothetical prote
39	19	100.0	79	ribosomal protein
40	19	100.0	81	T-cell receptor al
41	19	100.0	82	hypothetical prote
42	19	100.0	83	hypothetical prote
43	19	100.0	84	RPS34 protein homo
44	19	100.0	86	signal peptidase I
45	19	100.0	86	prostastic steroid-
46	19	100.0	90	hypothetical prote
47	19	100.0	92	conserved hypothet
48	19	100.0	91	hypothetical prote
49	19	100.0	91	RP534 protein homo
50	19	100.0	94	ribosomal protein
51	19	100.0	95	T-cell receptor al
52	19	100.0	96	hypothetical prote
53	19	100.0	97	hypothetical prote
54	19	100.0	97	hypothetical prote
55	19	100.0	99	hypothetical prote
56	19	100.0	99	ribosomal protein
57	19	100.0	100	transcription regu
58	19	100.0	100	hypothetical prote
59	19	100.0	101	Orf47 (bacteriopho
60	19	100.0	105	hydroxymethylgluta
61	19	100.0	105	hydroxymethylgluta
62	19	100.0	110	probable dihydron
63	19	100.0	110	T-cell receptor al
64	19	100.0	110	hypothetical prote
65	19	100.0	110	nonstructural prot
66	19	100.0	110	nonstructural prot
67	19	100.0	110	nonstructural prot
68	19	100.0	110	nonstructural prot
69	19	100.0	110	nonstructural prot
70	19	100.0	112	nonstructural prot
71	19	100.0	112	nonstructural prot
72	19	100.0	112	nonstructural prot
73	19	100.0	113	T-cell receptor al
74	19	100.0	116	hypothetical prote
75	19	100.0	116	hypothetical prote
76	19	100.0	116	abasic acid-indu
77	19	100.0	117	hypothetical prote
78	19	100.0	117	minor capsid prote
79	19	100.0	119	probable dihydron
80	19	100.0	120	dihydroneopterin a
81	19	100.0	120	T-cell receptor de
82	19	100.0	121	insertion sequence
83	19	100.0	122	ribosomal protein
84	19	100.0	122	hypothetical prote
85	19	100.0	122	cadmium-binding pr
86	19	100.0	122	hypothetical prote
87	19	100.0	123	probable dihydron
88	19	100.0	123	probable kinase Yg
89	19	100.0	123	probable kinase Yg
90	19	100.0	123	T-cell receptor de
91	19	100.0	124	probable trxA prot
92	19	100.0	126	H92967
93	19	100.0	127	CERF2V
94	19	100.0	128	G86629
95	19	100.0	128	transposase BMEL14
96	19	100.0	129	T-cell receptor de
97	19	100.0	130	D27974
98	19	100.0	131	A07873
99	19	100.0	131	D24092
100	19	100.0	131	S24092
101	19	100.0	133	S49487
102	19	100.0	133	G545893

103	19	100.0	134	2	S55890	176	19	100.0	190	2	A59418
104	19	100.0	135	2	T11489	177	19	100.0	190	2	GB5542
105	19	100.0	136	2	C90254	178	19	100.0	190	2	C90254
106	19	100.0	137	2	S03477	179	19	100.0	190	2	E44775
107	19	100.0	139	2	A7026	180	19	100.0	191	2	C64376
108	19	100.0	140	2	B95049	181	19	100.0	191	2	E85607
109	19	100.0	140	2	H97919	182	19	100.0	191	2	D90798
110	19	100.0	141	2	P10045	183	19	100.0	191	2	RDBPT4
111	19	100.0	142	2	D95237	184	19	100.0	193	2	T29706
112	19	100.0	142	2	E98101	185	19	100.0	193	2	T50787
113	19	100.0	142	2	D75134	186	19	100.0	194	2	S21859
114	19	100.0	143	2	JL0082	187	19	100.0	194	2	F64025
115	19	100.0	144	2	B30471	188	19	100.0	194	2	S39543
116	19	100.0	144	2	A86722	189	19	100.0	198	2	S12789
117	19	100.0	145	2	AC2572	190	19	100.0	198	2	F95139
118	19	100.0	146	2	B64246	191	19	100.0	199	2	E69756
119	19	100.0	146	2	B9424	192	19	100.0	199	2	F00542
120	19	100.0	146	2	AH2258	193	19	100.0	199	2	T20297
121	19	100.0	147	2	S76050	194	19	100.0	199	2	S12789
122	19	100.0	152	2	F86473	195	19	100.0	201	2	C97074
123	19	100.0	152	2	T06545	196	19	100.0	201	2	F69988
124	19	100.0	156	1	B64021	197	19	100.0	201	2	S21346
125	19	100.0	157	2	E97424	198	19	100.0	202	2	J01091
126	19	100.0	157	2	AD2442	199	19	100.0	203	2	T02868
127	19	100.0	158	2	E8691	200	19	100.0	203	2	J124042
128	19	100.0	159	2	AFT372	201	19	100.0	204	2	T50787
129	19	100.0	159	2	AD1742	202	19	100.0	204	2	S70149
130	19	100.0	159	2	A64672	203	19	100.0	204	2	T45948
131	19	100.0	159	2	H71845	204	19	100.0	205	2	S31127
132	19	100.0	159	2	H72279	205	19	100.0	205	2	T34375
133	19	100.0	160	2	H83673	206	19	100.0	205	2	T02868
134	19	100.0	160	2	AEB485	207	19	100.0	206	2	J01091
135	19	100.0	162	2	AB2644	208	19	100.0	207	2	T50787
136	19	100.0	164	2	H64669	209	19	100.0	207	2	H84610
137	19	100.0	164	2	D77845	210	19	100.0	207	2	T08520
138	19	100.0	165	2	D95600	211	19	100.0	207	2	S31128
139	19	100.0	165	2	H97142	212	19	100.0	208	2	AF3538
140	19	100.0	166	2	D30844	213	19	100.0	208	2	S49196
141	19	100.0	166	2	D87664	214	19	100.0	208	2	G34323
142	19	100.0	167	2	A35456	215	19	100.0	208	2	T03627
143	19	100.0	169	2	E85502	216	19	100.0	208	2	T01588
144	19	100.0	169	2	G77121	217	19	100.0	208	2	F64244
145	19	100.0	169	2	D97720	218	19	100.0	208	2	D64380
146	19	100.0	169	2	BB8571	219	19	100.0	208	2	D88961
147	19	100.0	169	2	B66806	220	19	100.0	209	2	A12592
148	19	100.0	169	2	PC143	221	19	100.0	209	2	C97375
149	19	100.0	170	2	G81375	222	19	100.0	209	2	C87530
150	19	100.0	170	2	E70219	223	19	100.0	209	2	DNA-invertase - En
151	19	100.0	171	2	PC0038	224	19	100.0	209	2	uracil phosphoribosyl transferase - K1
152	19	100.0	171	2	BB7628	225	19	100.0	210	2	uracil phosphoribosyl transferase - soyb
153	19	100.0	171	2	F99266	226	19	100.0	210	2	GTP-binding protein
154	19	100.0	171	2	D81278	227	19	100.0	214	2	GTP-binding protein
155	19	100.0	173	2	CB85459	228	19	100.0	214	2	GTP-binding protein
156	19	100.0	175	2	G95535	229	19	100.0	214	2	uracil phosphoribosyl transferase - K1
157	19	100.0	176	1	E44056	230	19	100.0	214	2	uracil phosphoribosyl transferase - K1
158	19	100.0	176	2	A95234	231	19	100.0	215	2	uracil phosphoribosyl transferase - K1
159	19	100.0	176	2	F99357	232	19	100.0	215	2	uracil phosphoribosyl transferase - K1
160	19	100.0	176	2	T249976	233	19	100.0	216	2	uracil phosphoribosyl transferase - K1
161	19	100.0	176	2	T25614	234	19	100.0	216	2	uracil phosphoribosyl transferase - K1
162	19	100.0	179	2	S64843	235	19	100.0	217	1	TISY
163	19	100.0	181	1	TISYB	236	19	100.0	217	2	trypsin inhibitor
164	19	100.0	181	2	T367597	237	19	100.0	217	2	trypsin inhibitor
165	19	100.0	182	2	F71063	238	19	100.0	217	2	trypsin inhibitor
166	19	100.0	182	2	G98468	239	19	100.0	219	2	trypsin inhibitor
167	19	100.0	183	2	JX311	240	19	100.0	220	1	trypsin inhibitor
168	19	100.0	183	2	S76453	241	19	100.0	220	1	trypsin inhibitor
169	19	100.0	186	2	T0911	242	19	100.0	220	2	trypsin inhibitor
170	19	100.0	186	2	A95234	243	19	100.0	220	2	trypsin inhibitor
171	19	100.0	187	2	F71063	244	19	100.0	224	1	trypsin inhibitor
172	19	100.0	189	2	AB5560	245	19	100.0	224	2	trypsin inhibitor
173	19	100.0	189	2	AB5560	246	19	100.0	224	2	trypsin inhibitor
174	19	100.0	190	2	A59410	247	19	100.0	224	2	trypsin inhibitor
175	19	100.0	190	2	A59410	248	19	100.0	224	2	trypsin inhibitor
176	19	100.0	190	2	G72163	249	19	100.0	224	2	trypsin inhibitor
177	19	100.0	190	2	WWRV1	250	19	100.0	224	2	trypsin inhibitor
178	19	100.0	190	2	F71934	251	19	100.0	224	2	trypsin inhibitor
179	19	100.0	190	2	F71934	252	19	100.0	224	2	trypsin inhibitor
180	19	100.0	190	2	F71934	253	19	100.0	224	2	trypsin inhibitor
181	19	100.0	190	2	F71934	254	19	100.0	224	2	trypsin inhibitor
182	19	100.0	190	2	F71934	255	19	100.0	224	2	trypsin inhibitor
183	19	100.0	190	2	F71934	256	19	100.0	224	2	trypsin inhibitor
184	19	100.0	190	2	F71934	257	19	100.0	224	2	trypsin inhibitor
185	19	100.0	190	2	F71934	258	19	100.0	224	2	trypsin inhibitor
186	19	100.0	190	2	F71934	259	19	100.0	224	2	trypsin inhibitor
187	19	100.0	190	2	F71934	260	19	100.0	224	2	trypsin inhibitor
188	19	100.0	190	2	F71934	261	19	100.0	224	2	trypsin inhibitor
189	19	100.0	190	2	F71934	262	19	100.0	224	2	trypsin inhibitor
190	19	100.0	190	2	F71934	263	19	100.0	224	2	trypsin inhibitor
191	19	100.0	190	2	F71934	264	19	100.0	224	2	trypsin inhibitor
192	19	100.0	190	2	F71934	265	19	100.0	224	2	trypsin inhibitor
193	19	100.0	190	2	F71934	266	19	100.0	224	2	trypsin inhibitor
194	19	100.0	190	2	F71934	267	19	100.0	224	2	trypsin inhibitor
195	19	100.0	190	2	F71934	268	19	100.0	224	2	trypsin inhibitor
196	19	100.0	190	2	F71934	269	19	100.0	224	2	trypsin inhibitor
197	19	100.0	190	2	F71934	270	19	100.0	224	2	trypsin inhibitor
198	19	100.0	190	2	F71934	271	19	100.0	224	2	trypsin inhibitor
199	19	100.0	190	2	F71934	272	19	100.0	224	2	trypsin inhibitor
200	19	100.0	190	2	F71934	273	19	100.0	224	2	trypsin inhibitor
201	19	100.0	190	2	F71934	274	19	100.0	224	2	trypsin inhibitor
202	19	100.0	190	2	F71934	275	19	100.0	224	2	trypsin inhibitor
203	19	100.0	190	2	F71934	276	19	100.0	224	2	trypsin inhibitor
204	19	100.0	190	2	F71934	277	19	100.0	224	2	trypsin inhibitor
205	19	100.0	190	2	F71934	278	19	100.0	224	2	trypsin inhibitor
206	19	100.0	190	2	F71934	279	19	100.0	224	2	trypsin inhibitor
207	19	100.0	190	2	F71934	280	19	100.0	224	2	trypsin inhibitor
208	19	100.0	190	2	F71934	281	19	100.0	224	2	trypsin inhibitor
209	19	100.0	190	2	F71934	282	19	100.0	224	2	trypsin inhibitor
210	19	100									

Protein Sequence Searches- February 2005

All of the sequence databases on ABS/S have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

Om protein - protein search, using sw model
Run on: May 19, 2006, 17:30:14 ; Search time 50 Seconds
Perfect score: US-10-825-958-13
Sequence: 1 KLVF 4
Scoring table: BLOSUM62
Gappen 10.0 , Gapext 0.5
Searched: 650591 seqs, 87530628 residues
Total number of hits satisfying chosen parameters: 650591
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

1: Issued_Patents_AA:/*
2: /EMC_Celerra_SIDS3/ptodata/2/1aa/5_COMBO.pep:/*
3: /EMC_Celerra_SIDS3/ptodata/2/1aa/7_COMBO.pep:/*
4: /EMC_Celerra_SIDS3/ptodata/2/1aa/H_COMBO.pep:/*
5: /EMC_Celerra_SIDS3/ptodata/2/1aa/PCTUS_COMBO.pep:/*
6: /EMC_Celerra_SIDS3/ptodata/2/1aa/RE_COMBO.pep:/*
7: /EMC_Celerra_SIDS3/ptodata/2/1aa/backfilesls1.pep:/*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Length	DB ID	Description
1	19	100.0	4	2 US-08-970-833-1
2	19	100.0	4	2 US-08-664-379B-17
3	19	100.0	4	2 US-09-095-106A-25
4	19	100.0	4	2 US-09-747-408-6
5	19	100.0	4	2 US-09-747-408-4
6	19	100.0	5	1 US-08-127-904-15
7	19	100.0	5	1 US-08-612-785B-10
8	19	100.0	5	2 US-09-970-833-2
9	19	100.0	5	2 US-08-703-675C-46
10	19	100.0	5	2 US-09-242-724-25
11	19	100.0	5	2 US-09-242-724-10
12	19	100.0	5	2 US-08-617-267C-10
13	19	100.0	5	2 US-08-617-267C-37
14	19	100.0	5	2 US-09-95-106A-1
15	19	100.0	5	2 US-09-095-106A-19
16	19	100.0	5	2 US-09-095-106A-33
17	19	100.0	5	2 US-09-747-408-8
18	19	100.0	5	2 US-09-747-408-15
19	19	100.0	5	5 PCT-US94-1047-5
20	19	100.0	6	1 US-08-612-785B-8
21	19	100.0	6	1 US-08-612-785B-9
22	19	100.0	6	1 US-08-612-785B-31
23	19	100.0	6	2 US-08-664-379B-19
24	19	100.0	6	2 US-08-703-675C-31
25	19	100.0	6	2 US-08-703-675C-32
26	19	100.0	6	2 US-08-703-675C-44
27	19	100.0	6	2 US-09-724-51-20
28	19	100.0	6	2 US-09-724-51-21
29	19	100.0	6	2 US-09-242-724-30
30	19	100.0	6	2 US-09-242-724-31
31	19	100.0	6	2 US-08-617-267C-8
32	19	100.0	6	2 US-08-617-267C-31
33	19	100.0	6	2 US-08-617-267C-6
34	19	100.0	6	2 US-08-617-267C-53
35	19	100.0	6	2 US-09-242-724-27
36	19	100.0	6	2 US-09-242-724-28
37	19	100.0	6	2 US-09-242-724-33
38	19	100.0	6	2 US-09-741-408-3
39	19	100.0	6	2 US-09-747-408-11
40	19	100.0	6	2 US-09-747-408-24
41	19	100.0	7	1 US-08-127-904-14
42	19	100.0	7	1 US-08-612-785B-6
43	19	100.0	7	1 US-08-612-785B-7
44	19	100.0	7	2 US-08-703-675C-29
45	19	100.0	7	2 US-08-703-675C-30
46	19	100.0	7	2 US-08-617-267C-6
47	19	100.0	7	2 US-08-617-267C-7
48	19	100.0	7	2 US-09-265-7091-13
49	19	100.0	7	2 US-09-095-106A-11
50	19	100.0	7	2 US-09-095-106A-12
51	19	100.0	7	2 US-09-747-408-2
52	19	100.0	7	2 US-09-747-408-18
53	19	100.0	7	2 US-09-747-408-19
54	19	100.0	7	2 US-08-457-804-1
55	19	100.0	7	2 US-08-457-804-5
56	19	100.0	8	1 US-08-457-804-7
57	19	100.0	8	1 US-08-457-804-11
58	19	100.0	8	1 US-08-612-785B-5
59	19	100.0	8	1 US-08-612-645-1
60	19	100.0	8	2 US-08-703-675C-28
61	19	100.0	8	2 US-08-617-267C-5
62	19	100.0	8	2 US-09-095-106A-8
63	19	100.0	8	2 US-09-095-106A-9
64	19	100.0	8	2 US-09-095-106A-44
65	19	100.0	8	2 US-08-765-96A-1
66	19	100.0	8	2 US-09-663-314C-73
67	19	100.0	8	5 PCT-US96-10220-1
68	19	100.0	9	2 US-09-264-709A-4
69	19	100.0	9	2 US-09-095-106A-6
70	19	100.0	9	2 US-09-095-106A-7
71	19	100.0	9	2 US-08-765-596A-53
72	19	100.0	9	2 US-08-765-596A-54
73	19	100.0	9	2 US-08-765-596A-64
74	19	100.0	9	2 US-09-747-408-20
75	19	100.0	10	2 US-08-970-833-3
76	19	100.0	10	2 US-09-095-106A-2
77	19	100.0	10	2 US-09-724-61-18
78	19	100.0	10	2 US-09-724-61-19
79	19	100.0	10	2 US-09-724-61-20
80	19	100.0	10	2 US-09-724-61-21
81	19	100.0	10	2 US-09-724-61-22
82	19	100.0	10	2 US-09-724-61-23
83	19	100.0	10	2 US-09-724-61-24
84	19	100.0	10	2 US-09-580-018-18
85	19	100.0	10	2 US-09-580-018-19
86	19	100.0	10	2 US-09-580-018-20
87	19	100.0	10	2 US-09-580-018-21
88	19	100.0	10	2 US-09-580-018-22
89	19	100.0	10	2 US-09-580-018-23
90	19	100.0	10	2 US-09-580-018-24
91	19	100.0	10	2 US-09-724-51-18
92	19	100.0	10	2 US-09-724-51-19
93	19	100.0	10	2 US-09-724-51-20
94	19	100.0	10	2 US-09-724-51-21
95	19	100.0	10	2 US-09-724-51-22
96	19	100.0	10	2 US-09-724-51-23
97	19	100.0	10	2 US-09-724-51-24
98	19	100.0	10	2 US-09-724-51-25
99	19	100.0	10	2 US-09-724-51-26

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GenCore version 5.1.8
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OM protein - protein search, using SW model
 Run on: May 19, 2006, 17:30:23 ; Search time 182 Seconds
 Perfect score: 19 KLVF 4

Sequence: 10.181 Million cell updates/sec
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqB, 463214858 residues
 Total number of hits satisfying chosen parameters: 2097797
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Listing first 1000 summaries

Database : Published Applications AA Main: *
 1: /EMC_Gelerra_SINS3/prodata/2/pubpaal/US07_PUBCOMB.pep: *
 2: /EMC_Gelerra_SINS3/prodata/2/pubpaal/US08_PUBCOMB.pep: *
 3: /EMC_Gelerra_SINS3/prodata/2/pubpaal/US09_PUBCOMB.pep: *
 4: /EMC_Gelerra_SINS3/prodata/2/pubpaal/US10_PUBCOMB.pep: *
 5: /EMC_Gelerra_SINS3/prodata/2/pubpaal/US11_PUBCOMB.pep: *
 6: /EMC_Gelerra_SINS3/prodata/2/pubpaal/US11_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	4	3 US-09-867-847-15	Sequence 15, Appli
2	19	100.0	4	3 US-09-867-847-23	Sequence 23, Appli
3	19	100.0	4	3 US-09-850-061A-25	Sequence 25, Appli
4	19	100.0	4	3 US-09-915-092-5	Sequence 5, Appli
5	19	100.0	4	3 US-09-915-092-13	Sequence 13, Appli
6	19	100.0	4	3 US-09-747-408-6	Sequence 6, Appli
7	19	100.0	4	3 US-09-747-408-14	Sequence 14, Appli
8	19	100.0	4	4 US-10-721-774-25	Sequence 25, Appli
9	19	100.0	4	5 US-10-728-028-5	Sequence 5, Appli
10	19	100.0	4	5 US-10-728-028-13	Sequence 13, Appli
11	19	100.0	4	5 US-10-825-958-13	Sequence 13, Appli
12	19	100.0	4	5 US-10-825-958-21	Sequence 21, Appli
13	19	100.0	4	5 US-10-665-091-2	Sequence 2, Appli
14	19	100.0	5	3 US-09-867-847-17	Sequence 17, Appli
15	19	100.0	5	3 US-09-867-847-25	Sequence 25, Appli
16	19	100.0	5	3 US-09-850-061A-1	Sequence 1, Appli
17	19	100.0	5	3 US-09-850-061A-19	Sequence 19, Appli
18	19	100.0	5	3 US-09-850-061A-43	Sequence 43, Appli
19	19	100.0	5	3 US-09-972-475-10	Sequence 10, Appli
20	19	100.0	5	3 US-09-972-475-37	Sequence 37, Appli
21	19	100.0	5	3 US-09-915-092-7	Sequence 7, Appli
22	19	100.0	5	3 US-09-915-092-15	Sequence 15, Appli
23	19	100.0	5	3 US-09-747-408-8	Sequence 8, Appli
24	19	100.0	5	3 US-09-747-408-16	Sequence 16, Appli
25	19	100.0	5	4 US-10-463-729-10	Sequence 10, Appli
26	19	100.0	5	4 US-10-463-729-37	Sequence 37, Appli
27	19	100.0	5	4 US-10-721-774-1	Sequence 1, Appli

100.0	19	100.0	5	4 US-10-721-774-19	Sequence 19, Appli
100.0	19	100.0	5	4 US-10-728-028-7	Sequence 43, Appli
100.0	19	100.0	5	4 US-10-728-028-7	Sequence 7, Appli
100.0	19	100.0	5	4 US-10-966-919B-4	Sequence 15, Appli
100.0	19	100.0	5	4 US-11-998-674-1	Sequence 1, Appli
100.0	19	100.0	5	4 US-10-825-958-23	Sequence 23, Appli
100.0	19	100.0	5	4 US-10-775-522-4	Sequence 4, Appli
100.0	19	100.0	5	4 US-10-666-055-1	Sequence 1, Appli
100.0	19	100.0	5	4 US-10-901-848B-1	Sequence 1, Appli
100.0	19	100.0	5	4 US-10-966-919B-4	Sequence 1, Appli
100.0	19	100.0	5	4 US-10-867-847-7	Sequence 7, Appli
100.0	19	100.0	5	4 US-09-867-847-20	Sequence 20, Appli
100.0	19	100.0	5	4 US-09-867-847-52	Sequence 52, Appli
100.0	19	100.0	5	4 US-09-867-847-55	Sequence 55, Appli
100.0	19	100.0	5	4 US-09-867-847-58	Sequence 58, Appli
100.0	19	100.0	5	4 US-09-867-847-61	Sequence 61, Appli
100.0	19	100.0	5	4 US-09-867-847-64	Sequence 64, Appli
100.0	19	100.0	6	3 US-09-850-061A-5	Sequence 5, Appli
100.0	19	100.0	6	3 US-09-850-061A-15	Sequence 15, Appli
100.0	19	100.0	6	3 US-09-956-625-25	Sequence 25, Appli
100.0	19	100.0	6	3 US-09-972-475-9	Sequence 9, Appli
100.0	19	100.0	6	3 US-09-972-475-31	Sequence 31, Appli
100.0	19	100.0	6	3 US-09-972-475-43	Sequence 43, Appli
100.0	19	100.0	6	3 US-09-915-092-10	Sequence 10, Appli
100.0	19	100.0	6	3 US-09-15-052-28	Sequence 28, Appli
100.0	19	100.0	6	3 US-10-463-729-9	Sequence 9, Appli
100.0	19	100.0	6	3 US-10-463-729-31	Sequence 31, Appli
100.0	19	100.0	6	3 US-10-463-729-43	Sequence 43, Appli
100.0	19	100.0	6	3 US-10-325-852-16	Sequence 16, Appli
100.0	19	100.0	6	4 US-10-721-774-5	Sequence 5, Appli
100.0	19	100.0	6	4 US-10-463-729-8	Sequence 8, Appli
100.0	19	100.0	6	4 US-10-463-729-9	Sequence 9, Appli
100.0	19	100.0	6	4 US-10-463-729-31	Sequence 31, Appli
100.0	19	100.0	6	4 US-10-463-729-43	Sequence 43, Appli
100.0	19	100.0	6	4 US-10-728-028-27	Sequence 27, Appli
100.0	19	100.0	6	4 US-10-728-028-28	Sequence 28, Appli
100.0	19	100.0	6	4 US-10-825-958-7	Sequence 7, Appli
100.0	19	100.0	6	4 US-10-825-958-18	Sequence 18, Appli
100.0	19	100.0	6	4 US-10-825-958-50	Sequence 50, Appli
100.0	19	100.0	6	5 US-10-825-958-53	Sequence 53, Appli
100.0	19	100.0	6	5 US-10-825-958-56	Sequence 56, Appli
100.0	19	100.0	6	5 US-10-825-958-62	Sequence 62, Appli
100.0	19	100.0	6	5 US-10-666-055-3	Sequence 3, Appli
100.0	19	100.0	7	3 US-09-867-847-12	Sequence 12, Appli
100.0	19	100.0	7	3 US-09-867-847-27	Sequence 27, Appli
100.0	19	100.0	7	3 US-09-867-847-28	Sequence 28, Appli
100.0	19	100.0	7	3 US-09-850-061A-11	Sequence 11, Appli
100.0	19	100.0	7	3 US-09-850-061A-12	Sequence 12, Appli
100.0	19	100.0	7	3 US-09-722-455-6	Sequence 6, Appli
100.0	19	100.0	7	3 US-09-972-475-7	Sequence 7, Appli
100.0	19	100.0	7	3 US-09-915-092-2	Sequence 2, Appli
100.0	19	100.0	7	3 US-09-915-092-17	Sequence 17, Appli
100.0	19	100.0	7	3 US-09-915-092-18	Sequence 18, Appli
100.0	19	100.0	7	3 US-09-747-408-2	Sequence 2, Appli
100.0	19	100.0	7	3 US-09-747-408-18	Sequence 18, Appli
100.0	19	100.0	7	3 US-09-747-408-19	Sequence 19, Appli
100.0	19	100.0	7	4 US-10-463-729-6	Sequence 6, Appli
100.0	19	100.0	7	4 US-10-463-729-7	Sequence 7, Appli
100.0	19	100.0	7	4 US-10-721-774-11	Sequence 11, Appli
100.0	19	100.0	7	4 US-10-721-774-12	Sequence 12, Appli
100.0	19	100.0	7	5 US-10-728-028-2	Sequence 2, Appli
100.0	19	100.0	7	5 US-10-728-028-17	Sequence 17, Appli
100.0	19	100.0	7	5 US-10-728-028-18	Sequence 18, Appli
100.0	19	100.0	7	5 US-10-825-958-10	Sequence 10, Appli
100.0	19	100.0	7	5 US-10-825-958-25	Sequence 25, Appli
100.0	19	100.0	7	5 US-10-825-958-26	Sequence 26, Appli
100.0	19	100.0	7	5 US-10-810-881A-18	Sequence 128, Appli
100.0	19	100.0	7	5 US-10-505-313-267	Sequence 267, Appli

Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 33, Appl